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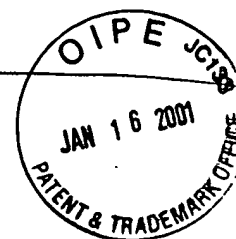
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SEQUENCE LISTING



<110> Estell, David A.

<120> Proteases From Gram-Positive Organisms

<130> GC381-US

<140> US 09/462,846

<141> 2000-01-13

<150> PCT/US98/19529

<151> 1998-07-14

<150> EP 97305227.7

<151> 1997-07-15

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<170> FastSEQ for Windows Version 3.0

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<212> PRT

<213> Bacillus subtilis

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Arg Thr Gly Glu Cys Trp Ala Phe Ala Ala His Gln Asn Gly Gln Ser
35 40 45

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TEBH CENTER 1600/2000

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				85					90					95	
His	Pro	Asn	Asp	Glu	Tyr	Ala	Asn	Ile	His	Glu	Asn	Gly	Glu	Leu	Gly
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Lys	Thr	Glu	Cys	Trp	Tyr	Ile	Ile	Asp	Cys	Gln	Lys	Asp	Ala	Glu	Ile
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Ile	Tyr	Gly	His	Asn	Ala	Thr	Thr	Lys	Glu	Glu	Leu	Thr	Thr	Met	Ile
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Gly	Ile	Leu	Ala	Leu	Glu	Thr	Gln	Gln	Asn	Ser	Asp	Thr	Thr	Tyr	Arg
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 <213> Bacillus subtilis

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Gln	Leu	Val	Ala	Gln	Tyr	Gly	Ile	His	Tyr	Arg	Asn	Thr	Tyr	Pro	Tyr
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Glu	Gly	Val	Gln	Arg	Tyr	Cys	Arg	Ser	Arg	Glu	Lys	Gly	Pro	Tyr	Ala
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 130 135 140
 Ala Gly Lys Asp Phe Gln Leu Tyr Arg Gly Gly Ile Phe Val Gly Pro
 145 150 155 160
 Cys Gly Asn Lys Val Asp His Ala Val Ala Val Gly Tyr Gly Pro
 165 170 175
 Asn Tyr Ile Leu Ile Lys Asn Ser Trp Gly Thr Gly Trp Gly Glu Asn
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 35 40 45
 Ser Thr Val Ala Asn Gly Pro Tyr Lys Gly Lys Thr Leu Ile Glu Leu
 50 55 60
 Trp Glu Glu His Arg Glu Val Phe Gly Gly Val Glu Gly Asp Arg Phe
 65 70 75 80
 Pro Leu Leu Thr Lys Leu Leu Asp Val Lys Glu Asp Thr Ser Ile Lys
 85 90 95
 Val His Pro Asp Asp Tyr Tyr Ala Gly Glu Asn Glu Glu Gly Glu Leu
 100 105 110
 Gly Lys Thr Glu Cys Trp Tyr Ile Ile Asp Cys Lys Glu Asn Ala Glu

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Ile	Ile Tyr Gly His Thr	Ala Arg Ser Lys Thr	Glu Leu Val Thr Met		
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Ile	Asn Ser Gly Asp Trp	Glu Gly Leu Leu Arg	Arg Ile Lys Ile Lys		
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Pro	Gly Asp Phe Tyr Tyr	Val Pro Ser Gly Thr	Leu His Ala Leu Cys		
	165	170	175		
Lys	Gly Ala Leu Val Leu	Glu Thr Gln Gln Asn	Ser Asp Ala Thr Tyr		
	180	185	190		
Arg	Val Tyr Asp Tyr Asp	Arg Leu Asp Ser Asn	Gly Ser Pro Arg Glu		
	195	200	205		
Leu	His Phe Ala Lys Ala	Val Asn Ala Ala Thr	Val Pro His Val Asp		
	210	215	220		
Gly	Tyr Ile Asp Glu Ser	Thr Glu Ser Arg Lys	Gly Ile Thr Ile Lys		
225	230	235	240		
Thr	Phe Val Gln Gly Glu	Tyr Phe Ser Val Tyr	Lys Trp Asp Ile Asn		
	245	250	255		
Gly	Glu Ala Glu Met Ala	Gln Asp Glu Ser Phe	Leu Ile Cys Ser Val		
	260	265	270		
Ile	Glu Gly Ser Gly Leu	Leu Lys Tyr Glu Asp	Lys Thr Cys Pro Leu		
	275	280	285		
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gattatgcaa	aactgcacga	aaatggcgac	cttggtaaaa	cggagtgtctg	gtatatcatt	360
gattgcaaa	atgacgccga	actaattttg	ggacatcatg	caagcacaaa	ggaagagttc	420
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gaccagggcc	aaaaaagaac	tcttcatata	gaaaaagcca	tggaagtcac	aacgataccg	660
catatcgata	aagtgcatac	accggaagta	aaagaagttg	gtaacgctga	gatcattgtt	720
tatgtgcaat	cagattatct	ctcagtgtac	aaatggaaga	ttagcggccg	agctgctttt	780
ccttcatatc	aaacctatct	gctggggagt	gttctgagcg	gatcaggacg	aatcataaat	840
aatgggtattc	agtatgaatg	caatgcaggc	tcacacttta	ttctgcctgc	gcattttgga	900
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<400> 7

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Gly	Thr	Leu	Val	Leu	Glu	Ile	Gln	Gln	Asn	Ser	Asp	Thr	Thr	Tyr	Arg	180	185	190
Val	Tyr	Asp	Tyr	Asp	Arg	Cys	Asn	Asp	Gln	Gly	Gln	Lys	Arg	Thr	Leu	195	200	205
His	Ile	Glu	Lys	Ala	Met	Glu	Val	Ile	Thr	Ile	Pro	His	Ile	Asp	Lys	210	215	220
Val	His	Thr	Pro	Glu	Val	Lys	Glu	Val	Gly	Asn	Ala	Glu	Ile	Ile	Val	225	230	235
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Arg	Ala	Ala	Phe	Pro	Ser	Tyr	Gln	Thr	Tyr	Leu	Leu	Gly	Ser	Val	Leu	260	265	270
Ser	Gly	Ser	Gly	Arg	Ile	Ile	Asn	Asn	Gly	Ile	Gln	Tyr	Glu	Cys	Asn	275	280	285
Ala	Gly	Ser	His	Phe	Ile	Leu	Pro	Ala	His	Phe	Gly	Glu	Phe	Thr	Ile	290	295	300
Glu	Gly	Thr	Cys	Glu	Phe	Met	Ile	Ser	His	Pro						305	310	315

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